

RAW SEQUENCE LISTING

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Application Serial Number: 10/696,708 A
Source: IFWO
Date Processed by STIC: 10/14/04

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IFWO

RAW SEQUENCE LISTING

DATE: 10/14/2004

PATENT APPLICATION: US/10/696,708A

TIME: 10:52:22

Input Set : A:\164seqlist.txt

Output Set: N:\CRF4\10142004\J696708A.raw

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3 <110> APPLICANT: Keating, Mark T.
4   Splawski, Igor
6 <120> TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
7   SYNDROME GENE
9 <130> FILE REFERENCE: 2323-164
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/696,708A
C--> 12 <141> CURRENT FILING DATE: 2003-10-30
14 <150> PRIOR APPLICATION NUMBER: US 09/735,995
15 <151> PRIOR FILING DATE: 2000-12-14
17 <150> PRIOR APPLICATION NUMBER: US 09/226,012
18 <151> PRIOR FILING DATE: 1999-01-06
20 <150> PRIOR APPLICATION NUMBER: 09/122,847
21 <151> PRIOR FILING DATE: 1998-07-27
23 <160> NUMBER OF SEQ ID NOS: 116
25 <170> SOFTWARE: PatentIn Ver. 2.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 3480
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(3477)
36 <400> SEQUENCE: 1
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38 Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Phe Leu Asp
39   1           5           10           15
41 acc atc atc cgc aag ttt gag ggc cag agc cgt aag ttc atc atc gcc   96
42 Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Ile Ile Ala
43   20           25           30
45 aac gct cgg gtg gag aac tgc gcc gtc atc tac tgc aac gac ggc ttc   144
46 Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly Phe
47   35           40           45
49 tgc gag ctg tgc ggc tac tcg cgg gcc gag gtg atg cag cga ccc tgc   192
50 Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro Cys
51   50           55           60
53 acc tgc gac ttc ctg cac ggg ccg cgc acg cag cgc cgc gct gcc gcg   240
54 Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala Ala
55   65           70           75           80
57 cag atc gcg cag gca ctg ctg ggc gcc gag gag cgc aaa gtg gaa atc   288
58 Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu Ile
59   85           90           95
61 gcc ttc tac cgg aaa gat ggg agc tgc ttc cta tgt ctg gtg gat gtg   336
62 Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp Val

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66	Val	Pro	Val	Lys	Asn	Glu	Asp	Gly	Ala	Val	Ile	Met	Phe	Ile	Leu	Asn	
67	115				120				125								
69	ttc	gag	gtg	gtg	atg	gag	aag	gac	atg	gtg	ggg	tcc	ccg	gct	cat	gac	432
70	Phe	Glu	Val	Val	Met	Glu	Lys	Asp	Met	Val	Gly	Ser	Pro	Ala	His	Asp	
71	130				135				140								
73	acc	aac	cac	cgg	ggc	ccc	ccc	acc	agc	tgg	ctg	gcc	cca	ggc	cgc	gcc	480
74	Thr	Asn	His	Arg	Gly	Pro	Pro	Thr	Ser	Trp	Leu	Ala	Pro	Gly	Arg	Ala	
75	145				150				155				160				
77	aag	acc	ttc	cgc	ctg	aag	ctg	ccc	gcg	ctg	ctg	gcg	ctg	acg	gcc	cgg	528
78	Lys	Thr	Phe	Arg	Leu	Lys	Leu	Pro	Ala	Leu	Leu	Ala	Leu	Thr	Ala	Arg	
79	165				170				175								
81	gag	tcg	tcg	gtg	cgg	tcg	ggc	ggc	gcg	ggc	gcg	ggc	gcc	ccg	ggg		576
82	Glu	Ser	Ser	Val	Arg	Ser	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Ala	Pro	Gly	
83	180				185				190								
85	gcc	gtg	gtg	gtg	gac	gtg	gac	ctg	acg	ccc	gcg	gca	ccc	agc	agc	gag	624
86	Ala	Val	Val	Val	Asp	Val	Asp	Leu	Thr	Pro	Ala	Ala	Pro	Ser	Ser	Glu	
87	195				200				205								
89	tcg	ctg	gcc	ctg	gac	gaa	gtg	aca	gcc	atg	gac	aac	cac	gtg	gca	ggg	672
90	Ser	Leu	Ala	Leu	Asp	Glu	Val	Thr	Ala	Met	Asp	Asn	His	Val	Ala	Gly	
91	210				215				220								
93	ctc	ggg	ccc	gcg	gag	gag	cgg	cgt	gcg	ctg	gtg	ggt	ccc	ggc	tct	ccg	720
94	Leu	Gly	Pro	Ala	Glu	Glu	Arg	Arg	Ala	Leu	Val	Gly	Pro	Gly	Ser	Pro	
95	225				230				235				240				
97	ccc	cgc	agc	gcg	ccc	ggc	cag	ctc	cca	tcg	ccc	cgg	gcg	cac	agc	ctc	768
98	Pro	Arg	Ser	Ala	Pro	Gly	Gln	Leu	Pro	Ser	Pro	Arg	Ala	His	Ser	Leu	
99	245				250				255								
101	aac	ccc	gac	gcc	tcg	ggc	tcc	agc	tgc	agc	ctg	gcc	cgg	acg	cgc	tcc	816
102	Asn	Pro	Asp	Ala	Ser	Gly	Ser	Ser	Cys	Ser	Leu	Ala	Arg	Thr	Arg	Ser	
103	260				265				270								
105	cga	gaa	agc	tgc	gcc	agc	gtg	cgc	cgc	gcc	tcg	tcg	gcc	gac	gac	atc	864
106	Arg	Glu	Ser	Cys	Ala	Ser	Val	Arg	Arg	Ala	Ser	Ser	Ala	Asp	Asp	Ile	
107	275				280				285								
109	gag	gcc	atg	cgc	gcc	ggg	gtg	ctg	ccc	ccg	cca	ccg	cgc	cac	gcc	agc	912
110	Glu	Ala	Met	Arg	Ala	Gly	Val	Leu	Pro	Pro	Pro	Pro	Arg	His	Ala	Ser	
111	290				295				300								
113	acc	ggg	gcc	atg	cac	cca	ctg	cgc	agc	ggc	ttg	ctc	aac	tcc	acc	tcg	960
114	Thr	Gly	Ala	Met	His	Pro	Leu	Arg	Ser	Gly	Leu	Leu	Asn	Ser	Thr	Ser	
115	305				310				315				320				
117	gac	tcc	gac	ctc	gtg	cgc	tac	cgc	acc	att	agc	aag	att	ccc	caa	atc	1008
118	Asp	Ser	Asp	Leu	Val	Arg	Tyr	Arg									

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131		370					375					380					
133	ctg	cct	gag	tac	aag	ctg	cag	gca	ccg	cgc	atc	cac	cgc	tgg	acc	atc	1200
134	Leu	Pro	Glu	Tyr	Lys	Leu	Gln	Ala	Pro	Arg	Ile	His	Arg	Trp	Thr	Ile	
135	385					390					395					400	
137	ctg	cat	tac	agc	ccc	ttc	aag	gcc	gtg	tgg	gac	tgg	ctc	atc	ctg	ctg	1248
138	Leu	His	Tyr	Ser	Pro	Phe	Lys	Ala	Val	Trp	Asp	Trp	Leu	Ile	Leu	Leu	
139					405					410					415		
141	ctg	gtc	atc	tac	acg	gct	gtc	ttc	aca	ccc	tac	tgc	gct	gcc	ttc	ctg	1296
142	Leu	Val	Ile	Tyr	Thr	Ala	Val	Phe	Thr	Pro	Tyr	Ser	Ala	Ala	Phe	Leu	
143				420					425					430			
145	ctg	aag	gag	acg	gaa	gaa	ggc	ccg	cct	gct	acc	gag	tgt	ggc	tac	gcc	1344
146	Leu	Lys	Glu	Thr	Glu	Glu	Gly	Pro	Pro	Ala	Thr	Glu	Cys	Gly	Tyr	Ala	
147			435					440					445				
149	tgc	cag	ccg	ctg	gct	gtg	gtg	gac	ctc	atc	gtg	gac	atc	atg	ttc	att	1392
150	Cys	Gln	Pro	Leu	Ala	Val	Val	Asp	Leu	Ile	Val	Asp	Ile	Met	Phe	Ile	
151		450					455					460					
153	gtg	gac	atc	ctc	atc	aac	ttc	cgc	acc	acc	tac	gtc	aat	gcc	aac	gag	1440
154	Val	Asp	Ile	Leu	Ile	Asn	Phe	Arg	Thr	Thr	Tyr	Val	Asn	Ala	Asn	Glu	
155	465					470					475					480	
157	gag	gtg	gtc	agc	cac	ccc	ggc	cgc	atc	gcc	gtc	cac	tac	ttc	aag	ggc	1488
158	Glu	Val	Val	Ser	His	Pro	Gly	Arg	Ile	Ala	Val	His	Tyr	Phe	Lys	Gly	
159					485					490					495		
161	tgg	ttc	ctc	atc	gac	atg	gtg	gcc	gcc	atc	ccc	ttc	gac	ctg	ctc	atc	1536
162	Trp	Phe	Leu	Ile	Asp	Met	Val	Ala	Ala	Ile	Pro	Phe	Asp	Leu	Leu	Ile	
163				500					505					510			
165	ttc	ggc	tct	ggc	tct	gag	gag	ctg	atc	ggg	ctg	ctg	aag	act	gcg	cgg	1584
166	Phe	Gly	Ser	Gly	Ser	Glu	Glu	Leu	Ile	Gly	Leu	Leu	Lys	Thr	Ala	Arg	
167			515					520					525				
169	ctg	ctg	cgg	ctg	gtg	cgc	gtg	gcg	cgg	aag	ctg	gat	cgc	tac	tca	gag	1632
170	Leu	Leu	Arg	Leu	Val	Arg	Val	Ala	Arg	Lys	Leu	Asp	Arg	Tyr	Ser	Glu	
171		530				535						540					
173	tac	ggc	gcg	gcc	gtg	ctg	ttc	ttg	ctc	atg	tgc	acc	ttt	gcg	ctc	atc	1680
174	Tyr	Gly	Ala	Ala	Val	Leu	Phe	Leu	Leu	Met	Cys	Thr	Phe	Ala	Leu	Ile	
175	545					550					555					560	
177	gcg	cac	tgg	cta	gcc	tgc	atc	tgg	tac	gcc	atc	ggc	aac	atg	gag	cag	1728
178	Ala	His	Trp	Leu	Ala	Cys	Ile	Trp	Tyr	Ala	Ile	Gly	Asn	Met	Glu	Gln	
179					565					570					575		
181	cca	cac	atg	gac	tca	cgc	atc	ggc	tgg	ctg	cac	aac	ctg	ggc	gac	cag	1776
182	Pro	His	Met	Asp	Ser	Arg	Ile	Gly	Trp	Leu	His	Asn	Leu	Gly	Asp	Gln	
183				580					585					590			
185	ata	ggc	aaa	ccc	tac	aac	agc	agc	ggc	ctg	ggc	ggc	ccc	tcc	atc	aag	1824
186	Ile	Gly	Lys	Pro	Tyr	Asn	Ser	Ser	Gly	Leu	Gly	Gly	Pro	Ser	Ile	Lys	
187			595					600					605				
189	gac	aag	tat	gtg	acg	gcg	ctc	tac	ttc	acc	ttc	agc	agc	ctc	acc	agt	1872
190	Asp	Lys	Tyr	Val	Thr	Ala	Leu	Tyr	Phe	Thr	Phe	Ser	Ser	Leu	Thr	Ser	
191		610					615					620					
193	gtg	ggc	ttc	ggc	aac	gtc	tct	ccc	aac	acc	aac	tca	gag	aag	atc	ttc	1920

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195	625				630					635						640	
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198	Ser	Ile	Cys	Val	Met	Leu	Ile	Gly	Ser	Leu	Met	Tyr	Ala	Ser	Ile	Phe	
199				645					650						655		
201	ggc	aac	gtg	tcg	gcc	atc	atc	cag	cgg	ctg	tac	tcg	ggc	aca	gcc	cgc	2016
202	Gly	Asn	Val	Ser	Ala	Ile	Ile	Gln	Arg	Leu	Tyr	Ser	Gly	Thr	Ala	Arg	
203				660					665					670			
205	tac	cac	aca	cag	atg	ctg	cgg	gtg	cgg	gag	ttc	atc	cgc	ttc	cac	cag	2064
206	Tyr	His	Thr	Gln	Met	Leu	Arg	Val	Arg	Glu	Phe	Ile	Arg	Phe	His	Gln	
207			675					680					685				
209	atc	ccc	aat	ccc	ctg	cgc	cag	cgc	ctc	gag	gag	tac	ttc	cag	cac	gcc	2112
210	Ile	Pro	Asn	Pro	Leu	Arg	Gln	Arg	Leu	Glu	Glu	Tyr	Phe	Gln	His	Ala	
211		690					695					700					
213	tgg	tcc	tac	acc	aac	ggc	atc	gac	atg	aac	gcg	gtg	ctg	aag	ggc	ttc	2160
214	Trp	Ser	Tyr	Thr	Asn	Gly	Ile	Asp	Met	Asn	Ala	Val	Leu	Lys	Gly	Phe	
215	705				710					715					720		
217	cct	gag	tgc	ctg	cag	gct	gac	atc	tgc	ctg	cac	ctg	aac	cgc	tca	ctg	2208
218	Pro	Glu	Cys	Leu	Gln	Ala	Asp	Ile	Cys	Leu	His	Leu	Asn	Arg	Ser	Leu	
219				725					730					735			
221	ctg	cag	cac	tgc	aaa	ccc	ttc	cga	ggg	gcc	acc	aag	ggc	tgc	ctt	cgg	2256
222	Leu	Gln	His	Cys	Lys	Pro	Phe	Arg	Gly	Ala	Thr	Lys	Gly	Cys	Leu	Arg	
223			740						745					750			
225	gcc	ctg	gcc	atg	aag	ttc	aag	acc	aca	cat	gca	ccg	cca	ggg	gac	aca	2304
226	Ala	Leu	Ala	Met	Lys	Phe	Lys	Thr	Thr	His	Ala	Pro	Pro	Gly	Asp	Thr	
227			755					760					765				
229	ctg	gtg	cat	gct	ggg	gac	ctg	ctc	acc	gcc	ctg	tac	ttc	atc	tcc	cgg	2352
230	Leu	Val	His	Ala	Gly	Asp	Leu	Leu	Thr	Ala	Leu	Tyr	Phe	Ile	Ser	Arg	
231		770					775					780					
233	ggc	tcc	atc	gag	atc	ctg	cgg	ggc	gac	gtc	gtc	gtg	gcc	atc	ctg	ggg	2400
234	Gly	Ser	Ile	Glu	Ile	Leu	Arg	Gly	Asp	Val	Val	Val	Ala	Ile	Leu	Gly	
235	785				790					795					800		
237	aag	aat	gac	atc	ttt	ggg	gag	cct	ctg	aac	ctg	tat	gca	agg	cct	ggc	2448
238	Lys	Asn	Asp	Ile	Phe	Gly	Glu	Pro	Leu	Asn	Leu	Tyr	Ala	Arg	Pro	Gly	
239				805					810					815			
241	aag	tcg	aac	ggg	gat	gtg	cgg	gcc	ctc	acc	tac	tgt	gac	cta	cac	aag	2496
242	Lys	Ser	Asn	Gly	Asp	Val	Arg	Ala	Leu	Thr	Tyr	Cys	Asp	Leu	His	Lys	
243			820						825					830			
245	atc	cat	cgg	gac	gac	ctg	ctg	gag	gtg	ctg	gac	atg	tac	cct	gag	ttc	2544
246	Ile	His	Arg	Asp	Asp	Leu	Leu	Glu	Val	Leu	Asp	Met	Tyr	Pro	Glu	Phe	
247			835					840					845				
249	tcc	gac	cac	ttc	tgg	tcc	agc	ctg	gag	atc	acc	ttc	aac	ctg	cga	gat	2592
250	Ser	Asp	His	Phe	Trp	Ser	Ser	Leu	Glu	Ile	Thr	Phe	Asn	Leu	Arg	Asp	
251		850					855					860					
253	acc	aac	atg	atc	ccg	ggc	tcc	ccc	ggc	agt	acg	gag	tta	gag	ggt	ggc	2640
254	Thr	Asn	Met	Ile	Pro	Gly	Ser	Pro	Gly	Ser	Thr	Glu	Leu	Glu	Gly	Gly	
255	865				870					875					880		
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263	900 905 910							
265	gcg ggg gca ggg ccg agt agc cgg ggc cgg ccg ggg ggg ccg tgg ggg	2784						
266	Ala Gly Ala Gly Pro Ser Ser Arg Gly Arg Pro Gly Gly Pro Trp Gly							
267	915 920 925							
269	gag agc ccg tcc agt ggc ccc tcc agc cct gag agc agt gag gat gag	2832						
270	Glu Ser Pro Ser Ser Gly Pro Ser Ser Pro Glu Ser Ser Glu Asp Glu							
271	930 935 940							
273	ggc cca ggc cgc agc tcc agc ccc ctc cgc ctg gtg ccc ttc tcc agc	2880						
274	Gly Pro Gly Arg Ser Ser Ser Pro Leu Arg Leu Val Pro Phe Ser Ser							
275	945 950 955 960							
277	ccc agg ccc ccc gga gag ccg ccg ggt ggg gag ccc ctg atg gag gac	2928						
278	Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met Glu Asp							
279	965 970 975							
281	tgc gag aag agc agc gac act tgc aac ccc ctg tca ggc gcc ttc tca	2976						
282	Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala Phe Ser							
283	980 985 990							
285	gga gtg tcc aac att ttc agc ttc tgg ggg gac agt cgg ggc cgc cag	3024						
286	Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly Arg Gln							
287	995 1000 1005							
289	tac cag gag ctc cct cga tgc ccc gcc ccc acc ccc agc ctc ctc aac	3072						
290	Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu Leu Asn							
291	1010 1015 1020							
293	atc ccc ctc tcc agc ccg ggt cgg cgg ccc cgg ggc gac gtg gag agc	3120						
294	Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp Val Glu Ser							
295	1025 1030 1035 1040							
297	agg ctg gat gcc ctc cag cgc cag ctc aac agg ctg gag acc cgg ctg	3168						
298	Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu Glu Thr Arg Leu							
299	1045 1050 1055							
301	agt gca gac atg gcc act gtc ctg cag ctg cta cag agg cag atg acg	3216						
302	Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu Gln Arg Gln Met Thr							
303	1060 1065 1070							
305	ctg gtc ccg ccc gcc tac agt gct gtg acc acc ccg ggg cct ggc ccc	3264						
306	Leu Val Pro Pro Ala Tyr Ser Ala Val Thr Thr Pro Gly Pro Gly Pro							
307	1075 1080 1085							
309	act tcc aca tcc ccg ctg ttg ccc gtc agc ccc ctc ccc acc ctc acc	3312						
310	Thr Ser Thr Ser Pro Leu Leu Pro Val Ser Pro Leu Pro Thr Leu Thr							
311	1090 1095 1100							
313	ttg gac tgc ctt tct cag gtt tcc cag ttc atg gcg tgt gag gag ctg	3360						
314	Leu Asp Ser Leu Ser Gln Val Ser Gln Phe Met Ala Cys Glu Glu Leu							
315	1105 1110 1115 1120							
317	ccc ccg ggg gcc cca gag ctt ccc caa gaa ggc ccc aca cga cgc ctc	3408						
318	Pro Pro Gly Ala Pro Glu Leu Pro Gln Glu Gly Pro Thr Arg Arg Leu							
319	1125 1130 1135							
321	tcc cta ccg ggc cag ctg ggg gcc ctc acc tcc cag ccc ctg cac aga	3456						
322	Ser Leu Pro Gly Gln Leu Gly Ala Leu Thr Ser Gln Pro Leu His Arg							
323	1140 1145 1150							

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date